



10

LINKS

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FEATURES             Location/Qualifiers
     source            1..1295
                        /organism="Homo sapiens"
                        /db_xref="taxon:9606"
                        /chromosome="17"
     gene              1..1295
                        /gene="LOC257238"
                        /db_xref="InterimID:257238"
     CDS               168..1295
                        /gene="LOC257238"
                        /cdon_start=1
                        /product="similar to cortical granule serine protease 1
                        precursor"
                        /protein_id="XP_011629.1"

```

note="Region: smart00020, Tryp_SPc, Trypsin-like serine protease; Many of these are synthesised as inactive precursor zymogens that are cleaved during limited proteolysis to generate their active forms. A few, however, are active as single chain molecules, and others are inactive due to substitutions of the catalytic triad residues"

misc_feature 171..434
gene="LOC257238"

misc_feature 819..1199
note="Region: pfam00089, trypsin, Trypsin"
gene="LOC257238"

misc_feature 900..1187
note="Region: pfam02395, IGA1, Immunoglobulin A1 protease. This family consists of immunoglobulin A1 protease proteins. The immunoglobulin A1 protease cleaves immunoglobulin IgA and is found in pathogenic bacteria such as *Neisseria gonorrhoeae*. Not all of the members of this family are IgA proteases (one member from *E. coli* cleaves human coagulation factor V, another one is a hemoglobin protease)"
gene="LOC257238"

misc_feature 903..1187
note="Region: smart00020, Tryp_SPc, Trypsin-like serine protease; Many of these are synthesised as inactive precursor zymogens that are cleaved during limited proteolysis to generate their active forms. A few, however, are active as single chain molecules, and others are inactive due to substitutions of the catalytic triad residues"

variation 681
gene="LOC257238"
allele="C"
allele="T"
db_xref="dbSNP:3742071"

BASE COUNT 352 a 265 c 314 g 364 t
ORIGIN

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121 tggttcatgt atgttgggga accttagtga gagagagcga tctttaaagc tggacagctg
181 tgaatgggaa taataatata catggagcgt atctcatalc caagaagata aaaattaaag
241 caatcattat tcatacaaac ttcatttttg aatcttatgt aaatgatatt gcacttttcc
301 acttaaaaaa agcagtggag tataatgact atattcagcc tatttgccca ccttttgatg
361 ttttccaaat cctggacgga aacacaaaag gttttataag tggctgggga agaacaaaag
421 aagaaggtat agcaggtctt gtgaactgtg tgtcctgtgg tctttacaag ctaaagtaca
481 gaadagatga gaaaatgtca attcatetta ttcacatgag agttctgtgc caaggatttg
541 ttgttggagc tgtgaactca gctcgacctt ttgcaggagg cgcacctgca atggccttac

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1261 ctttatgttt tgtcatttta cttagcaacaa cataa

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Revised: July 5, 2002.

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DocId:35013284

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Query: 215  GNATNILQDAEVHYISREMCNSERSYGGIIPNTSFCAGDEDGAFDTCRGDSGGPLMCYLP 274
           GNATNILQDAEVHYISREMCNSERSYGGIIPNTSFCAGDEDGAFDTCRGDSGGPLMCYLP
Sbjct: 900  GNATNILQDAEVHYISREMCNSERSYGGIIPNTSFCAGDEDGAFDTCRGDSGGPLMCYLP 1079

Query: 275  EYKRFVVMGITSYGHGCGREGFPGVYIGPSFYQKWLTEHFFHASTQGILTINILFGQILI 334
           EYKRFVVMGITSYGHGCGREGFPGVYIGPSFYQKWLTEHFFHASTQGILTINILFGQILI
Sbjct: 1080 EYKRFVVMGITSYGHGCGREGFPGVYIGPSFYQKWLTEHFFHASTQGILTINILFGQILI 1259

Query: 335  ALCFVILLATT 345
           ALCFVILLATT
Sbjct: 1260 ALCFVILLATT 1292

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>XM_171629 ACCESSION:XM_171629 NID: gi 22062231 ref XM_171629.1 Homo
sapiens similar to cortical granule serine protease 1
precursor (LOC257238), mRNA
Length = 1295

Identities = 141/153 (92%), Positives = 141/153 (92%)
Frame = +3

Query: 62 CGTAPLKDVLQGSRIIGSTEAGAGAWPWVSLQIKYGRVLVHVCGGTLVFERWVLTAAHC 121
CGTAPLKDVLQGSRIIGSTEAGAGAWPWVSLQIKYGRVLVHVCGGTLVFE
Sbjct: 3 CGTAPLKDVLQGSRIIGSTEAGAGAWPWVSLQIKYGRVLVHVCGGTLVFE----- 155
↓
Query: 122 TKDS DPLMWTAVIGTNNIHGRYPHTKKIKIKAI IHPNFILESYVNDIALFHLKKAVFYN 181
SDPLMWTAVIGTNNIHGRYPHTKKIKIKAI IHPNFILESYVNDIALFHLKKAVFYN
Sbjct: 156 ---SDPLMWTAVIGTNNIHGRYPHTKKIKIKAI IHPNFILESYVNDIALFHLKKAVFYN 326

Query: 182 DYIQPICLPFDV FQILDGNTKCFISGWGETKEE 214
DYIQPICLPFDV FQILDGNTKCFISGWGETKEE
Sbjct: 327 DYIQPICLPFDV FQILDGNTKCFISGWGETKEE 427

Identities = 131/131 (100%), Positives = 131/131 (100%)
Frame = +3

Query: 215 GNATNILQDAEVHYISREMCNUSERSYGGIIPNTSFCAGDEDGAFDTCFGDSSGGPLMCYLP 274
GNATNILQDAEVHYISREMCNUSERSYGGIIPNTSFCAGDEDGAFDTCFGDSSGGPLMCYLP
Sbjct: 900 GNATNILQDAEVHYISREMCNUSERSYGGIIPNTSFCAGDEDGAFDTCFGDSSGGPLMCYLP 1079

Query: 275 EYKRFFVMGITSYGHGCGRFGFPGVYIGPSFYQKWLTEHFFHASTQGILTINILRGQILI 334
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Sbjct: 1080 EYKRFFVMGITSYGHGCGRFGFPGVYIGPSFYQKWLTEHFFHASTQGILTINILRGQILI 1259

Query: 335 ALCFVILLATT 345
ALCFVILLATT
Sbjct: 1260 ALCFVILLATT 1292